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## SEQUENCE LISTING

&lt;110&gt; Julius-Maximilians-Universität Würzburg

&lt;120&gt; Millisecond activation switch for seven-transmembrane proteins

&lt;130&gt; H1340 PCT S3

&lt;150&gt; DE 102 59 874.6

&lt;151&gt; 2002-12-19

&lt;150&gt; EP 03 00 4394.7

&lt;151&gt; 2003-03-03

&lt;160&gt; 46

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 1409

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 1

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Val Cys Leu Ala Gly Leu Leu Met Leu Phe Thr Val Phe Gly Asn Val  
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Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu Lys Ala Pro Gln  
 65 70 75 80

Asn Leu Phe Leu Val Ser Leu Ala Ser Ala Asp Ile Leu Val Ala Thr  
 85 90 95

Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met Gly Tyr Trp Tyr  
 100 105 110

Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu Phe  
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Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr  
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Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg Thr Pro Arg  
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Arg Ile Lys Ala Ile Ile Val Thr Val Trp Val Ile Ser Ala Val Ile  
 165 170 175

Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly Ala Gly Gly Gly  
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Gln Gln Pro Ala Glu Pro Ser Cys Lys Ile Asn Asp Gln Lys Trp Tyr  
 195 200 205

Val Ile Ser Ser Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met  
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Ile Leu Val Tyr Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg  
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Val Pro Pro Ser Arg Arg Gly Pro Asp Ala Cys Ser Ala Pro Pro Gly  
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Gly Ala Asp Arg Arg Pro Asn Gly Leu Gly Pro Glu Arg Gly Ala Gly  
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Pro Thr Gly Ala Glu Ala Glu Pro Leu Pro Thr Gln Leu Asn Gly Ala  
 275 280 285

Pro Gly Glu Pro Ala Pro Ala Gly Pro Arg Asp Gly Asp Ala Leu Asp  
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Leu Glu Glu Ser Ser Ser Ser Glu His Ala Glu Arg Pro Pro Gly Pro  
 305 310 315 320

Arg Arg Pro Asp Arg Gly Pro Arg Ala Lys Gly Lys Thr Arg Ala Ser  
 325 330 335

Gln Val Lys Pro Gly Asp Ser Leu Pro Arg Arg Gly Pro Gly Ala Ala  
 340 345 350

Gly Pro Gly Ala Ser Gly Ser Gly His Gly Glu Glu Arg Gly Gly Gly  
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Ala Lys Ala Ser Arg Trp Arg Gly Arg Gln Asn Arg Glu Lys Arg Phe  
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Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Met
          20           25           30

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Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln Ala Gln Cys
35           40           45

```

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Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu
50           55           60

```

```

Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys
65           70           75           80

```

```

Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu
85           90           95

```

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Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp

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100

105

110

Asp His Ile Leu Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala  
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Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys Gly His Ala  
 130 135 140

Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Leu Val Pro Gly His  
 145 150 155 160

Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn  
 165 170 175

Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr  
 180 185 190

Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile  
 195 200 205

Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met  
 210 215 220

His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys  
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Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu  
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Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala  
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Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe  
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Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu  
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Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr  
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Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val  
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Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp  
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Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu  
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Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val  
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Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg  
 385 390 395 400

Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu  
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Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val  
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Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn  
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Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly  
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Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala  
 465 470 475 480

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr  
 485 490 495

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val  
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Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr  
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Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala  
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Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp  
 545 550 555 560

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser  
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Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val  
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&lt;211&gt; 391

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 6

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Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Ser Leu Ala  
 35 40 45

Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile Thr  
 50 55 60

Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile Ala  
 65 70 75 80

Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu Ala  
 85 90 95

Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr Asn  
 100 105 110

Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys Trp  
 115 120 125

Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn Asn  
 130 135 140

Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly Glu  
 145 150 155 160

Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr Met  
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Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu Met  
 180 185 190

Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys  
 195 200 205

Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr Leu

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210

215

220

Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly Leu  
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Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr Phe  
 245 250 255

Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu Ala  
 260 265 270

Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr Ala  
 275 280 285

Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg Ser  
 290 295 300

His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser Ala  
 305 310 315 320

Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu Arg  
 325 330 335

Leu Asn Gly His Pro Pro Gly Val Trp Ala Asn Gly Ser Ala Pro His  
 340 345 350

Pro Glu Arg Arg Pro Asn Gly Tyr Ala Leu Gly Leu Val Ser Gly Gly  
 355 360 365

Ser Ala Gln Glu Ser Gln Gly Asn Thr Gly Leu Pro Asp Val Glu Leu  
 370 375 380

Leu Ser His Glu Leu Lys Gly  
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&lt;210&gt; 7

&lt;211&gt; 720

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; eCFP (enhanced CFP) cDNA sequence

&lt;400&gt; 7

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&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; eCFP (enhanced CFP) amino acid sequence

&lt;400&gt; 8

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
          20          25          30

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
          35          40          45

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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
          50          55          60

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Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65          70          75          80

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Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
          85          90          95

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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
          100         105         110

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Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn  
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
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13/66

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser

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165

170

175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu  
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 225 230 235

&lt;210&gt; 11

&lt;211&gt; 2457

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; alpha2a adrenergic receptor-cam cDNA sequence

&lt;400&gt; 11

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15/66

tgcttcgccc gctaccccga ccacatgaag cagcacgact tcttcaagtc cgccatgccc 1020  
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 gccgaggtga agttcgaggg cgacaccctg gtgaaccgca tcgagctgaa gggcatcgac 1140  
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 gtctatatca tggccgacaa gcagaagaac ggcatcaagg tgaacttcaa gatccgccac 1260  
 aacatcgagg acggcagcgt gcagctcgcc gaccactacc agcagaacac ccccatcggc 1320  
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 gacccaacg agaagcgga tcacatggtc ctgctggagt tcgtgaccgc cgccgggatc 1440  
 actctcgga tggacgagct gtacaagcgc tggcgcgga ggcaaaaccg ggagaaacgc 1500  
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&lt;210&gt; 12

&lt;211&gt; 818

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; alpha 2a adrenergic receptor-cam "chameleon" amino acid sequence

16/66

&lt;400&gt; 12

Met Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Met Gly Ser Leu  
 1 5 10 15

Gln Pro Asp Ala Gly Asn Ser Ser Trp Asn Gly Thr Glu Ala Pro Gly  
 20 25 30

Gly Gly Thr Arg Ala Thr Pro Tyr Ser Leu Gln Val Thr Leu Thr Leu  
 35 40 45

Val Cys Leu Ala Gly Leu Leu Met Leu Phe Thr Val Phe Gly Asn Val  
 50 55 60

Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu Lys Ala Pro Gln  
 65 70 75 80

Asn Leu Phe Leu Val Ser Leu Ala Ser Ala Asp Ile Leu Val Ala Thr  
 85 90 95

Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met Gly Tyr Trp Tyr  
 100 105 110

Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu Phe  
 115 120 125

Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr  
 130 135 140

Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg Thr Pro Arg  
 145 150 155 160

Arg Ile Lys Ala Ile Ile Val Thr Val Trp Val Ile Ser Ala Val Ile  
 165 170 175

Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly Ala Gly Gly Gly  
 180 185 190

Gln Gln Pro Ala Glu Pro Ser Cys Lys Ile Asn Asp Gln Lys Trp Tyr  
 195 200 205

Val Ile Ser Ser Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met  
 210 215 220



17/66

Ile Leu Val Tyr Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg  
225 230 235 240

Val Pro Pro Ser Arg Arg Gly Pro Asp Ala Met Val Ser Lys Gly Glu  
245 250 255

Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp  
260 265 270

Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala  
275 280 285

Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu  
290 295 300

Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln  
305 310 315 320

Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys  
325 330 335

Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys  
340 345 350

Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
355 360 365

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
370 375 380

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
385 390 395 400

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Ash Phe  
405 410 415

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
420 425 430

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
435 440 445

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
450 455 460

18/66

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
 465 470 475 480

Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg Trp Arg Gly Arg Gln Asn  
 485 490 495

Arg Glu Lys Arg Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe  
 500 505 510

Val Val Cys Trp Phe Pro Phe Phe Thr Tyr Thr Leu Ile Ala Val  
 515 520 525

Gly Cys Pro Val Pro Ser Gln Leu Phe Asn Phe Phe Phe Trp Phe Gly  
 530 535 540

Tyr Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn His  
 545 550 555 560

Asp Phe Arg Arg Ala Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys  
 565 570 575

Arg Ile Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val  
 580 585 590

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser  
 595 600 605

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu  
 610 615 620

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu  
 625 630 635 640

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp  
 645 650 655

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr  
 660 665 670

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr  
 675 680 685

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu  
 690 695 700

19/66

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys  
705 710 715 720

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys  
725 730 735

Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu  
740 745 750

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile  
755 760 765

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln  
770 775 780

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu  
785 790 795 800

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu  
805 810 815

Tyr Lys

<210> 13  
<211> 2928  
<212> DNA  
<213> artificial sequence

<220>  
<223> PTH receptor-cam "chameleon" 8 cDNA sequence

<400> 13  
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ctgcaccgtg ctcaggccca gtgcgaaaaa cggctcaagg aggtcctgca gaggccagcc 180  
agcataatgg aatcagacaa gggatggaca tctgogtcca catcagggaa gcccaggaaa 240  
gataaggcat ctgggaagct ctaccctgag tctgaggagg acaaggaggc acccactggc 300  
agcagggtacc gagggcgccc ctgtctgccc gaatgggacc acatcctgtg ctggccgctg 360  
ggggcaccag gtgaggtggt ggctgtgccc tgtccggact acatttatga cttcaatcac 420  
aaaggccatg cctaccgacg ctgtgaccgc aatggcagct gggagctggt gcctgggcac 480

20/66

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cgggaggtgt ttgaccgcct gggcatgatt tacaccgtgg gctactccgt gtccctggcg	600
tccctcaccg tagctgtgct catcctggcc tacttttaggc ggctgcactg cacgcgcaac	660
tacatccaca tgcacctgtt cctgtccttc atgtgcgcgc ccgtgagcat cttcgtcaag	720
gacgctgtgc tctactctgg cgccacgctt gatgaggctg agcgccctcac cgaggaggag	780
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tgcagggttg ctgtgacctt cttcctttac ttcttgcca ccaactacta ctggattctg	900
gtggaggggc tgtacctgca cagcctcatc ttcatggcct tcttctcaga gaagaagtac	960
ctgtggggct tcacagtctt cggctggggg ctgcccgcgt tcttcgtggc tgtgtgggtc	1020
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tggatcatcc aggtgcccac cctggcctcc attgtgctca acttcatcct cttcatcaat	1140
atcgtccggg tgctcgccac caagctgcgc gagaccaacg ccggcatggg gagcaagggc	1200
gaggagctgt tcaccggggg ggtgcccatc ctggtcgagc tggacggcga cgtaaacggc	1260
cacaagttca gcgtgtccgg cgagggcgag ggcgatgcca cctacggcaa gctgaccctg	1320
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acctggggcg tgcaagtgtt cagccgctac cccgaccaca tgaagcagca cgacttcttc	1440
aagtccgcca tgcccgaagg ctacgtccag gagcgacca tcttcttcaa ggacgacggc	1500
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ttcaagatcc gccacaacat cgaggacggc agcgtgcagc tcgccgacca ctaccagcag	1740
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tccgccctga gcaaagaccc caacgagaag cgcgatcaca tggctcctgct ggagttcgtg	1860
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cagtaccgga agctgtctaa atccacgctg gtgctcatgc ccctcttttg cgtccactac	1980
attgtcttca tggccacacc atacaccgag gtctcaggga cgctctggca agtccagatg	2040
cactatgaga tgctcttcaa ctccctccag ggattttttg tcgcaatcat atactgtttc	2100
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21/66

```

ggccacaagt tcagcgtgtc cggcgagggc gagggcgatg ccacctacgg caagctgacc 2340
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ttcggctacg gcctgcagtg cttcgcccgc taccctgacc acatgaagca gcacgacttc 2460
ttcaagtccg ccatgcccgaggctacgtc caggagcgca ccatcttctt caaggacgac 2520
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gagctgaagg gcatcgactt caaggaggac ggcaacatcc tggggcaciaa gctggagtac 2640
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aacttcaaga tccgccaciaa catcgaggac ggagcgtgc agctcgccga ccaactaccag 2760
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cagtcgccc tgagcaaaga cccaacgag aagcgcgatc acatggtcct gctggagttc 2880
gtgaccgccg cgggatcac tctcgcatg gacgagctgt acaagtaa 2928

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&lt;210&gt; 14

&lt;211&gt; 975

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; PTH receptor-cam8 "chameleon" amino acid sequence

&lt;400&gt; 14

```

Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
1           5           10           15

```

```

Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Met
          20           25           30

```

```

Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln Ala Gln Cys
          35           40           45

```

```

Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu
50           55           60

```

```

Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys
65           70           75           80

```

```

Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu
          85           90           95

```

```

Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp

```

22/66

100					105					110					
Asp	His	Ile	Leu	Cys	Trp	Pro	Leu	Gly	Ala	Pro	Gly	Glu	Val	Val	Ala
		115					120					125			
Val	Pro	Cys	Pro	Asp	Tyr	Ile	Tyr	Asp	Phe	Asn	His	Lys	Gly	His	Ala
	130					135					140				
Tyr	Arg	Arg	Cys	Asp	Arg	Asn	Gly	Ser	Trp	Glu	Leu	Val	Pro	Gly	His
145					150					155					160
Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	Cys	Val	Lys	Phe	Leu	Thr	Asn
				165					170					175	
Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	Arg	Leu	Gly	Met	Ile	Tyr	Thr
			180					185					190		
Val	Gly	Tyr	Ser	Val	Ser	Leu	Ala	Ser	Leu	Thr	Val	Ala	Val	Leu	Ile
		195					200					205			
Leu	Ala	Tyr	Phe	Arg	Arg	Leu	His	Cys	Thr	Arg	Asn	Tyr	Ile	His	Met
	210					215					220				
His	Leu	Phe	Leu	Ser	Phe	Met	Leu	Arg	Ala	Val	Ser	Ile	Phe	Val	Lys
225					230					235					240
Asp	Ala	Val	Leu	Tyr	Ser	Gly	Ala	Thr	Leu	Asp	Glu	Ala	Glu	Arg	Leu
				245					250					255	
Thr	Glu	Glu	Glu	Leu	Arg	Ala	Ile	Ala	Gln	Ala	Pro	Pro	Pro	Pro	Ala
			260					265						270	
Thr	Ala	Ala	Ala	Gly	Tyr	Ala	Gly	Cys	Arg	Val	Ala	Val	Thr	Phe	Phe
	275						280					285			
Leu	Tyr	Phe	Leu	Ala	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	Val	Glu	Gly	Leu
	290					295					300				
Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	Glu	Lys	Lys	Tyr
305					310					315					320
Leu	Trp	Gly	Phe	Thr	Val	Phe	Gly	Trp	Gly	Leu	Pro	Ala	Val	Phe	Val
				325					330					335	

23/66

Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp  
 340 345 350

Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu  
 355 360 365

Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val  
 370 375 380

Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Met Val Ser Lys Gly  
 385 390 395 400

Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly  
 405 410 415

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp  
 420 425 430

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys  
 435 440 445

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Val  
 450 455 460

Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe  
 465 470 475 480

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe  
 485 490 495

Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly  
 500 505 510

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
 515 520 525

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His  
 530 535 540

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn  
 545 550 555 560

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp  
 565 570 575

24/66

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro  
580 585 590

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn  
595 600 605

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly  
610 615 620

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg Cys Asp Thr Arg Gln  
625 630 635 640

Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe  
645 650 655

Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser  
660 665 670

Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser  
675 680 685

Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu  
690 695 700

Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu  
705 710 715 720

Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr Gly  
725 730 735

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
740 745 750

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
755 760 765

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
770 775 780

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
785 790 795 800

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys  
805 810 815



25/66

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
820 825 830

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
835 840 845

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
850 855 860

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
865 870 875 880

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
885 890 895

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
900 905 910

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
915 920 925

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu  
930 935 940

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
945 950 955 960

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
965 970 975

<210> 15

<211> 2361

<212> DNA

<213> artificial sequence

<220>

<223> A2A-CFP14/10-YFP-C33 cDNA sequence; A2A "chameleon"

<400> 15

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accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc 180

ccctttgcca tcaccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt 240

26/66

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gaccgctaca ttgccatccg catcccgtc cggtacaatg gcttggtgac cggcacgagg	360
gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg	420
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ggcgacggcc ccgtgctgct gcccgacaac cactacctga gcaccagtc cgccctgagc	1260
aaagaccca acgagaagcg cgatcacatg gtctgtctgg agttcgtgac cgccgcccggg	1320
atcactctcg gcatggacga gctgtacaag cttcagaagg aggtccatgc tgccaagtca	1380
ctggccatca ttgtggggct ctttgccctc tgctggctgc ccctacacat catcaactgc	1440
ttcactttct tctgccccga ctgcagccac gccctctctt ggtcatgta cctggccatc	1500
gtcctctccc acaccaattc ggttgtgaat cccttcatct acgcctaccg tatccgcgag	1560
ttccgccaga ccttccgcaa gatcattcgc agccacgtcc tgaggcagca agaaccttc	1620
aaggcagctg gcaccagtc cggggtcgtg agcaagggcg aggagctgtt caccggggtg	1680
gtgcccattc tggtcgagct ggacggcgac gtaaaccggc acaagttcag cgtgtccggc	1740
gagggcgagg gcgatgccac ctacggcaag ctgaccctga agttcatctg caccaccggc	1800
aagctgcccg tgccctggcc caccctcgtg accaccttcg gctacggcct gcagtgttc	1860
gcccgctacc ccgaccacat gaagcagcac gacttcttca agtccgcat gccgaaggc	1920
tacgtccagg agcgcacat cttcttcaag gacgacggca actacaagac ccgcgccgag	1980
gtgaagttcg agggcgacac cctggtgaac cgcacgcagc tgaagggcat cgacttcaag	2040

27/66

gaggacggca acatcctggg gcacaagctg gagtacaact acaacagcca caacgtctat 2100  
 atcatggccg acaagcagaa gaacggcatc aaggtgaact tcaagatccg ccacaacatc 2160  
 gaggacggca gcgtgcagct cgccgaccac taccagcaga acacccccat cggcgacggc 2220  
 cccgtgctgc tgcccgacaa ccactacctg agctaccagt ccgccctgag caaagacccc 2280  
 aacgagaagc gcgatcacat ggtcctgctg gagttcgtga ccgccgccgg gatcactctc 2340  
 ggcatggacg agctgtacaa g 2361

<210> 16  
 <211> 784  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> A2A-CFP14/10-YFP-C33 amino acid sequence; "A2A chameleon"  
 <400> 16

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile  
 1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp  
 20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Ser Leu Ala  
 35 40 45

Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile Thr  
 50 55 60

Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile Ala  
 65 70 75 80

Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu Ala  
 85 90 95

Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr Asn  
 100 105 110

Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys Trp  
 115 120 125

Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn Asn  
 130 135 140

28/66

Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly Glu  
 145 150 155 160

Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr Met  
 165 170 175

Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu Met  
 180 185 190

Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys  
 195 200 205

Gln Met Glu Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro  
 210 215 220

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val  
 225 230 235 240

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys  
 245 250 255

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val  
 260 265 270

Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His  
 275 280 285

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val  
 290 295 300

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg  
 305 310 315 320

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu  
 325 330 335

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu  
 340 345 350

Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln  
 355 360 365

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp  
 370 375 380

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Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly  
 385 390 395 400

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser  
 405 410 415

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu  
 420 425 430

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr  
 435 440 445

Lys Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val  
 450 455 460

Gly Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe  
 465 470 475 480

Thr Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr  
 485 490 495

Leu Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile  
 500 505 510

Tyr Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile  
 515 520 525

Arg Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr  
 530 535 540

Ser Ala Arg Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 545 550 555 560

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 565 570 575

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 580 585 590

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 595 600 605

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro

30/66

610

615

620

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 625 630 635 640

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
 645 650 655

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 660 665 670

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 675 680 685

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 690 695 700

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 705 710 715 720

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 725 730 735

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr  
 740 745 750

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 755 760 765

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu  
 770 775 780

&lt;210&gt; 17

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 17

gtgcgtatatt accagatcgc caagcgtcgc acccgcgtgc ctcccagccg ccgggggtccg 60

gacgcctggt cgcgcgcgcc ggggggcgcc gatcgcaggc ccaacgggct gggcccggag 120

cgcgggcgcg gtccacggg cgctgaggcg gagccgctgc ccaccagct taacgggtgc 180

ccgggggagc ccgcgccgc cgggccccgc gatggggatg cgctggacct agaggagagt 240

tcgtcgtccg agcaagccga gcggccccgc gggccccgca gaccgaccg cggccccga 300

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gccaagggca agaccgggc gagtcaggtg aagccggggg acagtctgcc gcggcgcggg 360  
 cccggggccg cggggccggg ggcttcgggg tccgggcacg gagaggagcg cggcgggggc 420  
 gccaaagcgt cgcgctggcg cgggaggcaa aaccgggaga aacgcttcac gttcgtg 477

<210> 18  
 <211> 159  
 <212> PRT  
 <213> Mouse

<400> 18

Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg Val Pro Pro Ser  
 1 5 10 15

Arg Arg Gly Pro Asp Ala Cys Ser Ala Pro Pro Gly Gly Ala Asp Arg  
 20 25 30

Arg Pro Asn Gly Leu Gly Pro Glu Arg Gly Ala Gly Pro Thr Gly Ala  
 35 40 45

Glu Ala Glu Pro Leu Pro Thr Gln Leu Asn Gly Ala Pro Gly Glu Pro  
 50 55 60

Ala Pro Ala Gly Pro Arg Asp Gly Asp Ala Leu Asp Leu Glu Glu Ser  
 65 70 75 80

Ser Ser Ser Glu His Ala Glu Arg Pro Pro Gly Pro Arg Arg Pro Asp  
 85 90 95

Arg Gly Pro Arg Ala Lys Gly Lys Thr Arg Ala Ser Gln Val Lys Pro  
 100 105 110

Gly Asp Ser Leu Pro Arg Arg Gly Pro Gly Ala Ala Gly Pro Gly Ala  
 115 120 125

Ser Gly Ser Gly His Gly Glu Glu Arg Gly Gly Gly Ala Lys Ala Ser  
 130 135 140

Arg Trp Arg Gly Arg Gln Asn Arg Glu Lys Arg Phe Thr Phe Val  
 145 150 155

<210> 19  
 <211> 63  
 <212> DNA  
 <213> Mouse

32/66

<400> 19  
 cacgacttcc gacgcgcctt caagaagatc ctctgccgtg gggacagaaa acgcatcgtg 60

tga 63

<210> 20  
 <211> 20  
 <212> PRT  
 <213> Mouse

<400> 20

His Asp Phe Arg Arg Ala Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg  
 1 5 10 15

Lys Arg Ile Val  
 20

<210> 21  
 <211> 107  
 <212> DNA  
 <213> homo sapiens

<400> 21  
 ggatcttcct ggcggcgcgga cgacagctga agcagatgga gagccagcct ctgccggggg 60

agcgggcacg gtccacactg cagaaggagg tccatgctgc caagtca 107

<210> 22  
 <211> 36  
 <212> PRT  
 <213> homo sapiens

<400> 22

Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys Gln Met Glu Ser Gln  
 1 5 10 15

Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr Leu Gln Lys Glu Val His  
 20 25 30

Ala Ala Lys Ser  
 35

<210> 23  
 <211> 369  
 <212> DNA  
 <213> homo sapiens

<400> 23  
 cgtatccgcg agttccgcga gaccttcgcg aagatcattc gcagccacgt cctgaggcag 60



33/66

caagaacctt tcaaggcagc tggcaccagt gcccggtct tggcagctca tggcagtgac 120  
 ggagagcagg tcagcctccg tctcaacggc caccgccag gagtgtgggc caacggcagt 180  
 gctccccacc ctgagcggag gcccaatggc tatgccctgg ggctggtgag tggagggagt 240  
 gcccaagagt cccaggggaa cacgggcctc ccagacgtgg agctccttag ccatgagctc 300  
 aaggagtggt gccagagacc ccctggccta gatgaccccc tggcccagga tggagcagga 360  
 gtgtcctga 369

<210> 24  
 <211> 102  
 <212> PRT  
 <213> homo sapiens

<400> 24

Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg Ser His  
 1 5 10 15

Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser Ala Arg  
 20 25 30

Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu Arg Leu  
 35 40 45

Asn Gly His Pro Pro Gly Val Trp Ala Asn Gly Ser Ala Pro His Pro  
 50 55 60

Glu Arg Arg Pro Asn Gly Tyr Ala Leu Gly Leu Val Ser Gly Gly Ser  
 65 70 75 80

Ala Gln Glu Ser Gln Gly Asn Thr Gly Leu Pro Asp Val Glu Leu Leu  
 85 90 95

Ser His Glu Leu Lys Gly  
 100

<210> 25  
 <211> 57  
 <212> DNA  
 <213> homo sapiens

<400> 25  
 accaagctgc gggagaccaa cgccggccgg tgtgacacac ggcagcagta ccggaag 57

<210> 26  
 <211> 19

34/66

<212> PRT  
 <213> homo sapiens

<400> 26

Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln  
 1 5 10 15

Tyr Arg Lys

<210> 27  
 <211> 393  
 <212> DNA  
 <213> homo sapiens

<400> 27  
 gaggtacaag ctgagatcaa gaaatcttgg agccgctgga cactggcact ggacttcaag 60  
 cgaaaggcac gcagcgggag cagcagctat agctacggcc ccatggtgtc ccacacaagt 120  
 gtgaccaatg tcggcccccg tgtgggactc ggccctgcccc tcagcccccg cctactgccc 180  
 actgccacca ccaacggcca cctcagctg cctggccatg ccaagccagg gaccccagcc 240  
 ctggagaccc tcgagaccac accacctgcc atggctgctc ccaaggacga tgggttcctc 300  
 aacggctcct gctcaggcct ggacgaggag gcctctgggc ctgagcggcc acctgccttg 360  
 ctacaggaag agtgggagac agtcatgtga tga 393

<210> 28  
 <211> 129  
 <212> PRT  
 <213> homo sapiens

<400> 28

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala  
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr  
 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val  
 35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr  
 50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala  
 65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp  
85 90 95

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser  
100 105 110

Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val  
115 120 125

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<210> 29
<211> 264
<212> PRT
<213> artificial sequence
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<220>  
<223> PTHR-cam7 amino acid sequence

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala  
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Met Val Ser Lys Gly Glu Glu  
20 25 30

Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val  
35 40 45

Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr  
50 55 60

Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro  
65 70 75 80

Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	Gly	Tyr	Gly	Leu	Gln	Cys
				85					90					95	.

Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser  
100 105 110

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp  
115 120 125

36/66

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr  
 130 135 140

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly  
 145 150 155 160

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val  
 165 170 175

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys  
 180 185 190

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr  
 195 200 205

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn  
 210 215 220

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys  
 225 230 235 240

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr  
 245 250 255

Leu Gly Met Asp Glu Leu Tyr Lys  
 260

<210> 30

<211> 270

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam9 amino acid sequence

<400> 30

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala  
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Met  
 20 25 30

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 35 40 45

37/66

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 50 55 60

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 65 70 75 80

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 85 90 95

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln  
 100 105 110

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 115 120 125

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 130 135 140

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 145 150 155 160

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 165 170 175

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
 180 185 190

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val  
 195 200 205

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
 210 215 220

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser  
 225 230 235 240

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 245 250 255

Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 260 265 270

&lt;210&gt; 31

&lt;211&gt; 272

&lt;212&gt; PRT

38/66

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; PTHR-cam8 amino acid sequence

&lt;400&gt; 31

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala  
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr  
 20 25 30

Gly Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile  
 35 40 45

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser  
 50 55 60

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe  
 65 70 75 80

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr  
 85 90 95

Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met  
 100 105 110

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln  
 115 120 125

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala  
 130 135 140

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys  
 145 150 155 160

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu  
 165 170 175

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys  
 180 185 190

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly  
 195 200 205

39/66

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp  
 210 215 220

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala  
 225 230 235 240

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu  
 245 250 255

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 260 265 270

<210> 32

<211> 275

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam2 amino acid sequence

<400> 32

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala  
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr  
 20 25 30

Gly Pro Met Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
 35 40 45

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
 50 55 60

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
 65 70 75 80

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
 85 90 95

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro  
 100 105 110

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
 115 120 125

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys

40/66

130

135

140

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
 145 150 155 160

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
 165 170 175

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
 180 185 190

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
 195 200 205

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 210 215 220

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr  
 225 230 235 240

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 245 250 255

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu  
 260 265 270

Leu Tyr Lys  
 275

&lt;210&gt; 33

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; PTHR-cam5 amino acid sequence

&lt;400&gt; 33

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala  
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr  
 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val  
 35 40 45



41/66

Gly Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro  
 50 55 60

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val  
 65 70 75 80

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys  
 85 90 95

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val  
 100 105 110

Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His  
 115 120 125

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val  
 130 135 140

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg  
 145 150 155 160

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu  
 165 170 175

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu  
 180 185 190

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 195 200 205

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp  
 210 215 220

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly  
 225 230 235 240

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser  
 245 250 255

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu  
 260 265 270

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr

42/66

275

280

285

Lys

&lt;210&gt; 34

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; PTHR-caml amino acid sequence

&lt;400&gt; 34

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala  
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr  
 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val  
 35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr  
 50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala  
 65 70 75 80

Leu Glu Thr Leu Glu Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr  
 85 90 95

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His  
 100 105 110

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys  
 115 120 125

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp  
 130 135 140

Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg  
 145 150 155 160

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro  
 165 170 175

43/66

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn  
 180 185 190

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn  
 195 200 205

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu  
 210 215 220

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met  
 225 230 235 240

Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His  
 245 250 255

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn  
 260 265 270

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu  
 275 280 285

Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His  
 290 295 300

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met  
 305 310 315 320

Asp Glu Leu Tyr Lys  
 325

<210> 35

<211> 339

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam4 amino acid sequence

<400> 35

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala  
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr  
 20 25 30

44/66

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val  
35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr  
50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala  
65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp  
85 90 95

Asp Gly Phe Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val  
100 105 110

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe  
115 120 125

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr  
130 135 140

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr  
145 150 155 160

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro  
165 170 175

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly  
180 185 190

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys  
195 200 205

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile  
210 215 220

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His  
225 230 235 240

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp  
245 250 255

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile  
260 265 270

45/66

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro  
 275 280 285

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr  
 290 295 300

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val  
 305 310 315 320

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu  
 325 330 335

Leu Tyr Lys

<210> 36  
 <211> 354  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> PTHR-cam3 amino acid sequence

<400> 36

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala  
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr  
 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val  
 35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr  
 50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala  
 65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp  
 85 90 95

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser  
 100 105 110

46/66

Gly Pro Glu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val  
 115 120 125

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser  
 130 135 140

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu  
 145 150 155 160

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu  
 165 170 175

Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp  
 180 185 190

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr  
 195 200 205

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr  
 210 215 220

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu  
 225 230 235 240

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys  
 245 250 255

Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys  
 260 265 270

Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu  
 275 280 285

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile  
 290 295 300

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln  
 305 310 315 320

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu  
 325 330 335

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu  
 340 345 350

47/66

Tyr Lys

&lt;210&gt; 37

&lt;211&gt; 368

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; PTHR-caml0 amino acid sequence

&lt;400&gt; 37

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala  
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr  
 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val  
 35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr  
 50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala  
 65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp  
 85 90 95

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser  
 100 105 110

Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val  
 115 120 125

Met Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile  
 130 135 140

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser  
 145 150 155 160

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe  
 165 170 175

48/66

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr  
 180 185 190

Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met  
 195 200 205

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln  
 210 215 220

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala  
 225 230 235 240

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys  
 245 250 255

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu  
 260 265 270

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys  
 275 280 285

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly  
 290 295 300

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp  
 305 310 315 320

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala  
 325 330 335

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu  
 340 345 350

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 355 360 365

<210> 38

<211> 518

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-PTHR-FRETcontrol amino acid sequence

<400> 38



49/66

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala  
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Met Val Ser Lys Gly Glu Glu Leu  
 20 25 30

Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn  
 35 40 45

Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr  
 50 55 60

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val  
 65 70 75 80

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe  
 85 90 95

Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala  
 100 105 110

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp  
 115 120 125

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu  
 130 135 140

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn  
 145 150 155 160

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr  
 165 170 175

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile  
 180 185 190

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln  
 195 200 205

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His  
 210 215 220

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg  
 225 230 235 240

50/66

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu  
                   245                                  250                                  255

Gly Met Asp Glu Leu Tyr Lys Ser Gly Ser Ser Ser Tyr Ser Tyr Gly  
                   260                                  265                                  270

Pro Met Val Ser His Thr Ser Met Val Ser Lys Gly Glu Glu Leu Phe  
                   275                                  280                                  285

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly  
                   290                                  295                                  300

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly  
                   305                                  310                                  315                                  320

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro  
                                   325                                  330                                  335

Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser  
                   340                                  345                                  350

Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met  
                   355                                  360                                  365

Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly  
                   370                                  375                                  380

Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val  
                   385                                  390                                  395                                  400

Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile  
                                   405                                  410                                  415

Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile  
                   420                                  425                                  430

Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg  
                   435                                  440                                  445

His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln  
                   450                                  455                                  460

Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr  
                   465                                  470                                  475                                  480

51/66

Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp  
                   485                                  490                                  495

His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly  
                   500                                  505                                  510

Met Asp Glu Leu Tyr Lys  
                   515

<210> 39

<211> 1737

<212> DNA

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C49 cDNA sequence

<400> 39

```

atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc      60
atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc     120
accaactact ttgtggtgtc actggcgggc gccgacatcg cagtgggtgt gctcgccatc     180
ccctttgcca tcaccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt     240
gcctgcttcg tcctggtcct cagcgagagc tccatcttca gtctcctggc catcgccatt     300
gaccgctaca ttgccatccg catcccgtc cggtacaatg gcttggtgac cgggacgagg     360
gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg     420
ctaggttgga acaactgcgg tcagccaaag gagggcaaga accactccca gggctgcggg     480
gagggccaag tggcctgtct ctttgaggat gtggtcccca tgaactacat ggtgtacttc     540
aacttctttg cctgtgtgct ggtgcccctg ctgctcatgc tgggtgtcta tttgcggatc     600
ttcttggcgg cgcgacgaca gctgaagcag atggagagcc agtgttgtcc ggggtgttgt     660
gcacgggtcca cactgcagaa ggaggtccat gctgccaagt cactggccat cattgtgggg     720
ctctttgccc tctgttggtt gcccctacac atcatcaact gcttcacttt cttctgcccc     780
gactgcagcc acgcccctct ctgggtcatg tacctggcca tcgtcctctc ccacaccaat     840
tcggttgtga atcccttcat ctacgcctac cgtatccgcg agttccgcca gaccttccgc     900
aagatcattc gcagccacgt cctgaggcag caagaacctt tcaaggcagc tggcaccagt     960
gcccggttct tggcagctca tggcagtgac ggagagcagg tcagcctccg tctcaacggt    1020
gtgagcaagg gcgaggagct gttcaccggg gtggtgcccc tcctggtcga gctggacggc    1080

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52/66

gacgtaaacy gccacaggtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc 1140  
 aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gcccaccctc 1200  
 gtgaccaccc tgacctgggg cgtgcagtgc ttcagccgct accccgacca catgaagcag 1260  
 cacgacttct tcaagtccgc catgcccga ggtacgtcc aggagcgtac catcttcttc 1320  
 aaggacgacg gcaactacaa gaccgcgcgc gaggtgaagt tcgagggcga caccctgggtg 1380  
 aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag 1440  
 ctggagtaca actacatcag ccacaacgtc tatatcaccg ccgacaagca gaagaacggc 1500  
 atcaaggccc acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 1560  
 cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgccga caaccactac 1620  
 ctgagcaccc agtccgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg 1680  
 ctggagttcg tgaccgcgcg cgggatcact ctcggcatgg acgagctgta caagtaa 1737

&lt;210&gt; 40

&lt;211&gt; 578

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; A2A-FlashPG-CFP-C49 amino acid sequence

&lt;400&gt; 40

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile  
 1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp  
 20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu  
 35 40 45

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile  
 50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile  
 65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu  
 85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr  
 100 105 110

53/66

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys  
 115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn  
 130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly  
 145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr  
 165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu  
 180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu  
 195 200 205

Lys Gln Met Glu Ser Gln Cys Cys Pro Gly Cys Cys Ala Arg Ser Thr  
 210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly  
 225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr  
 245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu  
 260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr  
 275 280 285

Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg  
 290 295 300

Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser  
 305 310 315 320

Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu  
 325 330 335

Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val

54/66

340

345

350

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser  
 355 360 365

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu  
 370 375 380

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu  
 385 390 395 400

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp  
 405 410 415

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr  
 420 425 430

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr  
 435 440 445

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu  
 450 455 460

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys  
 465 470 475 480

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys  
 485 490 495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu  
 500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile  
 515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln  
 530 535 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu  
 545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu  
 565 570 575

55/66

Tyr Lys

&lt;210&gt; 41

&lt;211&gt; 1686

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; A2A-FlashPG-CFP-C33 cDNA sequence

&lt;400&gt; 41

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atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc      60
atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc     120
accaactact ttgtggtgtc actggcgggc gccgacatcg cagtgggtgt gctcgccatc     180
ccctttgcca tcaccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt     240
gcctgcttcg tcctggtcct cacgcagagc tccatcttca gtctcctggc catcgccatt     300
gaccgctaca ttgccatccg catcccgtc cggtacaatg gcttggtgac cgggacgagg     360
gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg     420
ctaggttgga acaactgcgg tcagccaaag gagggcaaga accactcca gggctgcggg     480
gagggccaag tggcctgtct ctttgaggat gtggtcccca tgaactacat ggtgtacttc     540
aacttctttg cctgtgtgct ggtgcccctg ctgctcatgc tgggtgtcta tttgcggatc     600
ttcctggcgg cgcgacgaca gctgaagcag atggagagcc agtgttgctc ggggtgttgt     660
gcacggtcca cactgcagaa ggaggccat gctgccaaagt cactggccat cattgtgggg     720
ctctttgccc tctgctggct gccctacac atcatcaact gcttcacttt cttctgcccc     780
gactgcagcc acgcccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat     840
tcggttggtga atcccttcat ctacgcctac cgtatccgcg agttccgcca gaccttccgc     900
aagatcattc gcagccacgt cctgaggcag caagaacctt tcaaggcagc tggcaccagt     960
gcccggtcgg tgagcaaggg cgaggagctg ttcaccgggg tggtgcccat cctggtcgag    1020
ctggacggcg acgtaaacgg ccacagggtc agcgtgtccg gcgagggcga gggcgatgcc    1080
acctacggca agctgaccct gaagttcatc tgcaccaccg gcaagctgcc cgtgccctgg    1140
cccaccctcg tgaccaccct gacctggggc gtgcagtgtc tcagccgcta ccccgaccac    1200
atgaagcagc acgacttctt caagtccgcc atgccgaag gctacgtcca ggagcgtacc    1260
atcttcttca aggacgacgg caactacaag acccgcgccg aggtgaagtt cgagggcgac    1320
accctggtga accgcatcga gctgaagggc atcgacttca aggaggacgg caacatcctg    1380

```

56/66

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gggcacaagc tggagtacaa ctacatcagc cacaacgtct atatcaccgc cgacaagcag 1440
aagaacggca tcaaggccca cttcaagatc cgccacaaca tcgaggacgg cagcgtgcag 1500
ctcgccgacc actaccagca gaacaccccc atcggcgacg gccccgtgct gctgcccagc 1560
aaccactacc tgagcaccca gtccgccttg agcaaagacc ccaacgagaa gcgcgatcac 1620
atggtcctgc tggagttcgt gaccgcccgc gggatcactc tcggcatgga cgagctgtac 1680
aagtaa 1686

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<210> 42
<211> 561
<212> PRT
<213> artificial sequence

<220>
<223> A2A-FlashPG-CFP-C33 amino acid sequence

<400> 42

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```

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
1           5           10           15

```

```

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
          20           25           30

```

```

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu
          35           40           45

```

```

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
          50           55           60

```

```

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
65           70           75           80

```

```

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
          85           90           95

```

```

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
          100          105          110

```

```

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
          115          120          125

```

```

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
          130          135          140

```



57/66

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly  
 145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr  
 165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu  
 180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu  
 195 200 205

Lys Gln Met Glu Ser Gln Cys Cys Pro Gly Cys Cys Ala Arg Ser Thr  
 210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly  
 225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr  
 245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu  
 260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr  
 275 280 285

Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg  
 290 295 300

Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser  
 305 310 315 320

Ala Arg Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro  
 325 330 335

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val  
 340 345 350

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys  
 355 360 365

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val  
 370 375 380

58/66

Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His  
385 390 395 400

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val  
405 410 415

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg  
420 425 430

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu  
435 440 445

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu  
450 455 460

Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln  
465 470 475 480

Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp  
485 490 495

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly  
500 505 510

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser  
515 520 525

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu  
530 535 540

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr  
545 550 555 560

Lys

&lt;210&gt; 43

&lt;211&gt; 1788

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; A2A-CFP-ModelPG-C49 cDNA sequence

&lt;400&gt; 43

atgcccatca tgggctcttc ggtgtacatc acgggtggagc tggccattgc tgtgctggcc

60

59/66

atcctgggca	atgtgctggt	gtgctgggcc	gtgtggetca	acagcaacct	gcagaacgtc	120
accaactact	ttgtgggtgc	actggcgggc	gccgacatcg	cagtgggtgt	gctcgccatc	180
ccctttgcc	tcaccatcag	caccgggttc	tgcgtgcct	gccacggctg	cctcttcatt	240
gcctgcttcg	tcctgggtcct	cacgcagagc	tccatcttca	gtctcctggc	catcgccatt	300
gaccgctaca	ttgccatccg	catcccgctc	cgggtacaatg	gcttgggtgac	cggcacgagg	360
gctaagggca	tcattgccat	ctgctgggtg	ctgtcgtttg	ccatcggcct	gactcccatg	420
ctaggttga	acaactgcgg	tcagccaaag	gagggcaaga	accactcca	gggctgcggg	480
gagggccaag	tggcctgtct	ctttgaggat	gtggtcccca	tgaactacat	ggtgtacttc	540
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60/66

<210> 44  
 <211> 595  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> A2A-CFP-ModelPG-C49 amino acid sequence

<400> 44

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Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu  
 35 40 45

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile  
 50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile  
 65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu  
 85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr  
 100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys  
 115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn  
 130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly  
 145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr  
 165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu  
 180 185 190

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Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu  
 195 200 205

Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr  
 210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly  
 225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr  
 245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu  
 260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr  
 275 280 285

Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg  
 290 295 300

Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser  
 305 310 315 320

Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu  
 325 330 335

Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val  
 340 345 350

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser  
 355 360 365

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu  
 370 375 380

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu  
 385 390 395 400

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp  
 405 410 415

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr  
 420 425 430

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Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr  
 435 440 445

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu  
 450 455 460

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys  
 465 470 475 480

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys  
 485 490 495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu  
 500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile  
 515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln  
 530 535 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu  
 545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu  
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Tyr Lys Ala Glu Ala Ala Ala Arg Glu Ala Cys Cys Pro Gly Cys Cys  
 580 585 590

Ala Arg Ala  
 595

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 <213> artificial sequence

<220>  
 <223> A2A-CFP-C49 cDNA sequence

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 accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc 180

63/66

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gaccgctaca ttgccatccg catcccgtc cggtacaatg gcttggtgac cggcacgagg 360
gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg 420
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&lt;210&gt; 46

&lt;211&gt; 578

&lt;212&gt; PRT

&lt;213&gt; artificial sequence

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&lt;220&gt;

&lt;223&gt; A2A-CFP-C49 amino acid sequence

&lt;400&gt; 46

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Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp  
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Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu  
 35 40 45

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile  
 50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile  
 65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu  
 85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr  
 100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys  
 115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn  
 130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly  
 145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr  
 165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu  
 180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu  
 195 200 205

Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr  
 210 215 220



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Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly  
 225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr  
 245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu  
 260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr  
 275 280 285

Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg  
 290 295 300

Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser  
 305 310 315 320

Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu  
 325 330 335

Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val  
 340 345 350

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser  
 355 360 365

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu  
 370 375 380

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu  
 385 390 395 400

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp  
 405 410 415

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr  
 420 425 430

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr  
 435 440 445

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu

66/66

450

455

460

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys  
465 470 475 480

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys  
485 490 495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu  
500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile  
515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln  
530 535 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu  
545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu  
565 570 575

Tyr Lys

50/66

51/66